

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 17:48:35 ; Search time 42 Seconds

(without alignments)  
929.299 Million cell updates/sec

Title: US-09-782-587b-1

Perfect score: 2187  
Sequence: 1 AANAFLXXLRPGSLXKRCXXX.....LQKLRSEPPRGVLLRAPPP 406

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

PIR.73: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2167	99.1	466	1 KFH07	coagulation factor
2	1601	72.2	443	2 I46937	coagulation factor
3	1566	71.6	407	1 KFB07	coagulation factor
4	858.5	39.3	475	1 EXCH	coagulation factor
5	858.5	39.3	488	1 EXHU	coagulation factor
6	850.5	38.9	416	1 KFB0	coagulation factor
7	849	38.8	461	1 KFHU	coagulation factor
8	843	38.5	492	1 EXBO	coagulation factor
9	831.5	38.0	482	1 EXRT	coagulation factor
10	824	37.7	459	2 J00419	coagulation factor
11	821	37.5	452	1 A30351	coagulation factor
12	781	33.7	159	2 I84615	coagulation factor
13	775	35.4	461	1 S18994	coagulation factor
14	769	35.2	461	1 JX0210	coagulation factor
15	749	34.2	456	1 KXBO	coagulation factor
16	726	33.2	461	1 KXHU	coagulation factor
17	519.5	23.8	275	2 I46712	coagulation factor
18	515.5	23.6	282	2 I84621	coagulation factor
19	513.5	23.5	271	2 I46580	coagulation factor
20	511	23.4	285	2 I48144	coagulation factor
21	509.5	23.3	274	2 I47078	coagulation factor
22	473	21.6	638	1 K0K5PL	coagulation factor
23	461.5	21.1	638	1 K0K5PL	coagulation factor
24	459.5	21.0	638	1 K0K5PL	coagulation factor
25	445.5	20.4	638	1 K0K5PL	coagulation factor
26	444	20.3	625	1 KFHU1	coagulation factor
27	443.5	20.3	622	1 TBHU	coagulation factor
28	439.5	20.1	655	1 A46688	coagulation factor
29	428.5	19.6	625	1 TBBO	coagulation factor

30	428	19.6	1035	1 A43090	enteropeptidase (E
31	426.5	19.5	246	1 TRRT1	trypsin (EC 3.4.21
32	425.5	19.5	618	2 A35827	thrombin (EC 3.4.21
33	423	19.3	229	1 TRDES	trypsin (EC 3.4.21
34	423	19.3	358	2 JC5878	plasma hyaluronan-
35	421	19.3	617	2 S10511	thrombin (EC 3.4.21
36	420.5	19.2	247	2 A27547	trypsin (EC 3.4.21
37	418	19.1	1019	1 A56318	enteropeptidase (E
38	417	19.1	786	1 A47547	serine proteinase
39	417	19.1	1034	1 A53663	enteropeptidase (E
40	416.5	19.0	246	1 TRRT2	trypsin (EC 3.4.21
41	415.5	19.0	855	2 JC7731	membrane-bound arg
42	415.5	19.0	855	2 JC7731	membrane-bound arg
43	413	18.9	417	1 S00845	hepsin (EC 3.4.21
44	412.5	18.9	248	2 S55066	trypsin (EC 3.4.21
45	411	18.8	810	2 I46260	plasmin (EC 3.4.21

#### ALIGNMENTS

RESULT 1  
KFH07  
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1989 #sequence, revision 19-May-1994 #text, change 08-Dec-2000  
C:Accession: A28322; A23819; A31186; B31186; S63524  
R:O'Hara, P.J.; Grant, F.J.; Haldean, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; M  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep  
A:Reference number: A28322; MUID:87260948; PMID:3037537  
A:Accession: A28322  
A:Molecule type: DNA  
A:Residues: 1-466 <OH>  
A:Cross-references: GB:J02933; NID:9180333; PIDN:AA51983.1; PID:9180334  
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A:Title: Characterization of a cDNA coding for human factor VII.  
A:Reference number: A23819; MUID:86205965; PMID:3486420  
A:Accession: A23819  
A:Molecule type: mRNA  
A:Residues: 1-466 <HAG>  
A:Cross-references: GB:M13232; NID:9182799; PIDN:AA88040.1; PID:9182801  
R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen,  
Biochemistry 27, 7785-7793, 1988  
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-  
A:Reference number: A90539; MUID:8908153; PMID:3264725  
A:Accession: A31186  
A:Molecule type: protein  
A:Residues: 61-212 <THR>  
A:Accession: B31186  
A:Molecule type: protein  
A:Residues: 213-466 <THR>  
R:Bjorn, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Pe  
J. Biol. Chem. 266, 11051-11057, 1991  
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylation  
A:Reference number: A40529; MUID:91250411; PMID:1904059  
A:Contents: annotation; carbohydrate binding sites  
R:Peterson, E.; Petersen, L.C.  
Eur. J. Biochem. 234, 293-300, 1995  
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-car  
A:Reference number: S63524; MUID:96096752; PMID:8529655  
A:Accession: S63524  
A:Molecule type: protein  
A:Residues: 61-65; 99-103; 105-109; 213-217; 308-312 <PER>  
C:Genetics:  
A:Gene: GDB:F7  
A:Cross-references: GDB:119897; OMIM:227500  
A:Map position: 13q34-13q34  
A:Intons: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr  
coagulation factor IX in the presence of calcium and tissue factor

A: Pathway: blood coagulation extrinsic pathway  
 C: Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C: Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
 F: 1-20/Domain: signal sequence #status predicted <SIG>  
 F: 21-60/Domain: propeptide #status predicted <PRO>  
 F: 45-104/Domain: Gla domain homology <GLA>  
 F: 61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>  
 F: 110-141/Domain: EGF homology <EG1>  
 F: 151-187/Domain: EGF homology <EG2>  
 F: 213-447/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
 F: 213-447/Domain: trypsin homology <TRY>  
 F: 66, 67, 74, 76, 79, 80, 85, 86, 89, 95/Modified site: gamma-carboxylglutamic acid (Glu) #status  
 F: 77-82, 110-121, 115-130, 132-141, 151-162, 158-172, 174-187, 195-322, 219-224, 238-254, 370-389,  
 F: 112, 120/Binding site: carboxylate (Ser) (covalent) #status experimental  
 F: 123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
 F: 205, 383/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F: 213-213/Cleavage site: Arg-His (coagulation factor XIIIa) #status experimental  
 F: 253, 302, 404/Active site: His, Asp, Ser #status predicted  
 F: 350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 99.1%; Score 2167; DB 1; Length 466;

Best Local Similarity 97.5%; Pred. No. 4, 4e-154; Mismatches 10; Indels 0; Gaps 0;

Matches 396; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRCKKXKXOCSEFXARXIFKDAKRTKLFWISYSDGQACASSPCQNGS 60  
 DB 61 ANAFLEELRPGSLRECKEELCSFEAREVEFQSTERTKQFWITNDGQACASSPCQNGS 120  
 QY 61 CKDOLQSTICCLAFEBERNETHKDDOLICVNEGCGEOYCSHTGKRCRCHEGYSL 120  
 DB 121 CKDOLQSTICCLAFEBERNETHKDDOLICVNEGCGEOYCSHTGKRCRCHEGYSL 180  
 QY 121 LADGVSCTPTVEYPCGKPILEKRNASKPGRIYGGKCPGECPMOVLVNGAQLCGG 180  
 DB 181 LADGVSCTPTVEYPCGKPILEKRNASKPGRIYGGKCPGECPMOVLVNGAQLCGG 240  
 QY 181 TLINTIWWVSAHCFDKIKNRNLIJAVGEHDLSEHDEGDSRRVAYIIPSTVPGTTN 240  
 DB 241 TLINTIWWVSAHCFDKIKNRNLIJAVGEHDLSEHDEGDSRRVAYIIPSTVPGTTN 300  
 QY 241 HDIALRLRHPVLTLDHVPPLCLPERFSESTLAFVRSLSVSGMQLDRATALEMVL 300  
 DB 301 HDIALRLRHPVLTLDHVPPLCLPERFSESTLAFVRSLSVSGMQLDRATALEMVL 360  
 QY 301 NVPLRLMODCLOQSRKVDSPNITEYMFACYSKSGKSGDGGSPGPHATYRGTWYLTG 360  
 DB 361 NVPLRLMODCLOQSRKVDSPNITEYMFACYSKSGKSGDGGSPGPHATYRGTWYLTG 420  
 QY 361 IVSMGCGATVGHGCVYTRVSOYIEMWLQKLMSRSEPRPVLLRAPPP 406  
 DB 421 IVSMGCGATVGHGCVYTRVSOYIEMWLQKLMSRSEPRPVLLRAPPP 466

# RESULT 2

146932  
 C: Species: Oryctolagus cuniculus (domestic rabbit)  
 C: Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text-change 12-Feb-1999  
 C: Accession: I46932  
 R: Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.  
 A: Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
 A: Reference number: I46932; MUID: 93190306; PMID: 8383365  
 A: Accession: I46932  
 A: Status: preliminary; translated from GB/EMBL/DBJ  
 A: Molecule type: mRNA  
 A: Residues: 1-443 <BRO>  
 C: Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 F: 24-83/Domain: Gla domain homology <GLA>  
 F: 89-120/Domain: EGF homology <EG1>  
 F: 130-166/Domain: EGF homology <EG2>  
 F: 192-425/Domain: trypsin homology <TRY>

Query Match 73.2%; Score 1601; DB 2; Length 443;  
 Best Local Similarity 71.4%; Pred. No. 6, 4e-112; Mismatches 72; Indels 2; Gaps 2;  
 Matches 290; Conservative 42; Mismatches 72; Indels 2; Gaps 2;

QY 1 ANAFLLXLRPGSLRCKKXKXOCSEFXARXIFKDAKRTKLFWISYSDGQACASSPCQNGS 60  
 DB 40 ANAFLEELRPGSLRECKEELCSFEAREVEFQSTERTKQFWITNDGQACASSPCQNGS 99  
 QY 61 CKDOLQSTICCLAFEBERNETHKDDOLICVNEGCGEOYCSHTGKRCRCHEGYSL 120  
 DB 100 CKDOLQSTICCLAFEBERNETHKDDOLICVNEGCGEOYCSHTGKRCRCHEGYSL 159  
 QY 121 LADGVSCTPTVEYPCGKPILEKRNASKPGRIYGGKCPGECPMOVLVNGAQLCGG 180  
 DB 160 LADGVSCTPTVEYPCGKPILEKRNASKPGRIYGGKCPGECPMOVLVNGAQLCGG 219  
 QY 181 TLINTIWWVSAHCFDKIKNRNLIJAVGEHDLSEHDEGDSRRVAYIIPSTVPGTTN 240  
 DB 220 TLINTIWWVSAHCFDKIKNRNLIJAVGEHDLSEHDEGDSRRVAYIIPSTVPGTTN 279  
 QY 241 HDIALRLRHPVLTLDHVPPLCLPERFSESTLAFVRSLSVSGMQLDRATALEMVL 300  
 DB 280 HDIALRLRHPVLTLDHVPPLCLPERFSESTLAFVRSLSVSGMQLDRATALEMVL 339  
 QY 301 NVPLRLMODCLOQSRKVDSPNITEYMFACYSKSGKSGDGGSPGPHATYRGTWYLTG 360  
 DB 340 NVPLRLMODCLOQSRKVDSPNITEYMFACYSKSGKSGDGGSPGPHATYRGTWYLTG 398  
 QY 361 IVSMGCGATVGHGCVYTRVSOYIEMWLQKLMSRSEPRPVLLRAPPP 406  
 DB 399 IVSMGCGATVGHGCVYTRVSOYIEMWLQKLMSRSEPRPVLLRAPPP 443

# RESULT 3

KB07  
 C: Species: Bos primigenius taurus (cattle)  
 C: Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text-change 16-Jul-1999  
 C: Accession: A31979; C20274  
 R: Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
 J. Biol. Chem. 263, 14868-14877, 1988  
 A: Title: Bovine factor VII. Its purification and complete amino acid sequence.  
 A: Reference number: A31979; MUID: 890808362; PMID: 3049594  
 A: Accession: A31979  
 A: Molecule type: protein  
 A: Residues: 1-407 <TAK>  
 R: McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A: Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood  
 A: Reference number: A20274; MUID: 83308813; PMID: 6688526  
 A: Accession: C20274  
 A: Molecule type: protein  
 A: Residues: 58-62, 'X', 64-68 <MCN>  
 A: Note: the residue designated 'X' was determined to be hydroxyaspartic acid  
 R: Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.  
 J. Biochem. 104, 867-868, 1988  
 A: Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c  
 A: Reference number: A44556; MUID: 89213999; PMID: 3149637  
 A: Accession: A44556  
 A: Contents: annotation  
 A: Note: structure and location of covalently bound carbohydrate  
 C: Function:  
 A: Description: catalyzes the proteolytic activation of coagulation factor X in the pr  
 A: Pathway: blood coagulation extrinsic pathway  
 C: Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 C: Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglu  
 F: 1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>  
 F: 1-44/Domain: Gla domain homology (fragment) <GLA>  
 F: 50-81/Domain: EGF homology <EG1>  
 F: 91-127/Domain: EGF homology <EG2>  
 F: 153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
 F: 153-387/Domain: trypsin homology <TRY>



A: Molecule type: mRNA  
 A: Residues: 1-488 <MES>  
 A: Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:9182390  
 R:Maio, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.  
 J. Biol. Chem. 267, 7395-7401, 1992  
 A: Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation factor  
 A: Reference number: A42485; MUID:92218390; PMID:1313796  
 A: Accession: A42485  
 A: Molecule type: DNA  
 A: Residues: 1-15 <MIN>  
 A: Experimental source: liver  
 A: Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)  
 R:Raul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
 Gene 4, 311-314, 1986  
 A: Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
 A: Reference number: A25853; MUID:86221713; PMID:3011603  
 A: Accession: A25853  
 A: Molecule type: mRNA  
 A: Residues: 13-284, 'E', 289-488 <KAD>  
 A: Cross-references: GB:M2613; NID:9180335; PIDN:AAA51984.1; PID:9180336  
 R:Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
 A: Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X  
 A: Reference number: A22208; MUID:85216545; PMID:2582420  
 A: Accession: A22208  
 A: Molecule type: mRNA  
 A: Residues: 13-441, 'S', 443-488 <EUN>  
 A: Cross-references: GB:K03194; NID:9182840; PIDN:AAA52490.1; PID:9182841  
 R:Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
 A: Title: Characterization of a cDNA coding for human factor X.  
 A: Reference number: A21284; MUID:84222026; PMID:6587384  
 A: Accession: A21284  
 A: Molecule type: mRNA  
 A: Residues: 13-284, 'E', 289-488 <LE2>  
 A: Cross-references: GB:K01886  
 R:McMillen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss  
 Biochemistry 22, 2875-2884, 1983  
 A: Title: Complete amino acid sequence of the light chain of human blood coagulation factor X  
 A: Reference number: A20362; MUID:83257207; PMID:6671167  
 A: Accession: A20362  
 A: Molecule type: protein  
 A: Residues: 41-179 <MCM>  
 R:Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A: Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X  
 A: Reference number: S39414; MUID:94062825; PMID:8243461  
 A: Accession: S39415  
 A: Molecule type: protein  
 A: Residues: 183-234 <INO>  
 A: Note: glycosylation sites  
 A: Note: identification and characterization of beta-hydroxyaspartic acid  
 R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.  
 Gene 84, 517-519, 1989  
 A: Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human blood coagulation factor X  
 A: Reference number: I54051; MUID:90128299; PMID:2612918  
 A: Accession: I54051  
 A: Status: translation not shown; translated from GB/EMBL/DBJ  
 A: Molecule type: DNA  
 A: Residues: 1-23 <RES>  
 A: Cross-references: GB:M33297; NID:9183860; PIDN:AAA5236.1; PID:9553330  
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Ble  
 J. Mol. Biol. 232, 947-966, 1993  
 A: Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
 A: Reference number: A49458; MUID:93360277; PMID:8355279  
 A: Contents: annotation: X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-c  
 C:Genetics: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
 A: Gene: GDB:F10  
 A: Cross-references: GDB:119890; OMTW:227600  
 A: Map position: 13q34-13q4  
 A: Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1

A: Note: deficiency of this factor causes Stuart disease  
 A: Description: catalyzes the proteolytic activation of prothrombin to thrombin in the  
 A: Pathway: blood coagulation  
 C: Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin hom  
 C: Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxygl  
 F: 1-23/Domain: signal sequence #status predicted <SIG>  
 F: 24-40/Domain: propeptide #status predicted <PRO>  
 F: 25-84/Domain: Gla domain homology <GLA>  
 F: 41-179/Domain: EGF homology <EGF>  
 F: 90-121/Domain: EGF homology <EG1>  
 F: 129-164/Domain: EGF homology <EG2>  
 F: 183-488/Domain: EGF homology <EG3>  
 F: 183-234/Domain: coagulation factor X heavy chain #status experimental <LCH>  
 F: 235-488/Domain: coagulation factor X heavy chain #status experimental <HCH>  
 F: 235-488/Domain: coagulation factor X heavy chain #status experimental <ACT>  
 F: 235-488/Domain: trypsin homology <TRY>  
 F: 46/47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu)  
 F: 57-62/Disulfide bonds: #status predicted  
 F: 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-342, 241-246, 261-277, 390-404, 415-  
 F: 103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F: 199, 211/Binding site: carbohydrate (Thn) (covalent) #status experimental  
 F: 221, 231/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F: 234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa)  
 F: 276, 322, 419/Active site: His, Asp, Ser #status experimental

Query Match 39.38; Score 858.5; DB 1; Length 488;  
 Best Local Similarly 37.18; Pred. No. 1.5e-56;  
 Matches 168; Conservative 76; Mismatches 146; Indels 63; Gaps 8;  
 1 ANAFLLXRLRGSLKRXCKXXXCFXKXARXIFKXAKRKLWISISDQDCASSPCQNGS 60  
 41 ANSLFEMKRGHLERECMEETGSEAEFEVDSKNEFNWKNKDKDQCTSPCQNGK 100  
 61 CKDOLSYICFCLPAEGRNCE--THKDDOLICNENGGEGEYOCSDHTGTRKRCHEGY 118  
 101 CKDGLGYTCTCLGFEGRKNCLEFTRK-----LCLDNGDCDDQCHEQNSV--VCSARGY 155  
 119 SLADVSCPTPEYVPCGKPILEKRNASKPQG----- 151  
 156 TLADNGKACIPTPYPCGK-OTLERRKRSVAQNTSSGSEAPDSITMKPYDAADLPENP 214  
 152 -----RIVGKVCPRKECQVOLL--VNGAQLCGGLTINTVVA 191  
 215 FDLIDNNOPTPERGDNNTTRIVGGOEKDECEWALLINENDEFCGFTILSEFYLLTA 274  
 192 AHCFIDKIKWRNLIAVLGEHDLSEHDGDECSRVAOVIIPTSTVPGTNNDIALLRHOP 251  
 275 AHCLYAKRKR---VAVGDRNTEDEEGEVAHEVEYVIAKHNRTKETEDYDIAVLRKTP 331  
 252 VLTIDHVPCLPTEPESERTLAIVRFPSVSGWGLLDRCATALELVLPRLMTODCL 311  
 332 IFPRMVAVACLPEROMASTLMTOKTGVSGGRHNKROSTRLKMLEVPYVDRNSC- 390  
 312 QOSRKVGDSPNTEYFCAGYSDGSKDSCGDSGGRHATYRGTWYLTGIVSGOCATV 371  
 391 ---KLSSEFIITONNFCAGYDTPKQEDACGSGGPHVRFKDYFTVGTIVSGECAR 446  
 372 GHGVYTRVSOYIEWLOKLMRSEPRPGVLLRAP 404  
 447 GKGYITTKVATFLKIDRSMKTRGCPKAKSHAP 479

RESULT 6  
 KEBO  
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
 N: Alternate names: Christmas factor  
 C: Species: Bos primigenius taurus (cattle)  
 C: Date: 30-Nov-1980 #sequence, revision 03-Aug-1984 #text, change 16-Jul-1999  
 C: Accession: A14757; B20274; I45891; A00923  
 R: Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.;  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979  
 A: Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas  
 A: Reference number: A14757; MUID:80056619; PMID:291916

A:Accession: A14757  
 A:Molecule type: protein  
 A:Residues: 1-63, 'T', '65-416 <KAT>  
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX  
 A:Reference number: A20774; PMID:83308813; PMID:6688526  
 A:Accession: B20774  
 A:Molecule type: protein  
 A:Residues: 59-63, 'X', '65-69 <MCM>  
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.  
 Nature 299, 178-180, 1982  
 A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX  
 A:Reference number: 145891; PMID:82272386; PMID:6287289  
 A:Accession: 145891  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 52-139 <CHO>  
 A:Cross-references: GB:J00007; NID:q163053; PIND:AAA30520.1; PID:q163054  
 R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Biochem. 104, 867-868, 1988  
 A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IX  
 A:Reference number: A44556; PMID:89213999; PMID:3149637  
 A:Contents: annotation  
 A:Note: structure and location of a carbohydrate covalently bound to Ser C:Comment: Factor IX is activated by factor X<sub>IIa</sub>, which excises the activation peptide p C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the pres A:Pathway: blood coagulation intrinsic pathway  
 A:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 A:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam F:1-16/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F:1-45/Domain: Gla domain homology (fragment) <GLA>  
 F:51-82/Domain: EGF homology <EG1>  
 F:88-124/Domain: EGF homology <EG2>  
 F:147-181/Domain: activation peptide #status experimental <APT>  
 F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:182-409/Domain: trypsin homology <TRY>  
 F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #str F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,133-299,207-223,337-351,362-390/Dsulfide F:53/Binding site: carboxylate (Ser) (covalent) #status experimental  
 F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:158,166,173,261/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 38.9%; Score 850.5; DB 1; Length 416;  
 Best Local Similarity 40.2%; Pred. No. 5; 1e-56;  
 Matches 167; Conservative 68; Mismatches 129; Indels 51; Gaps 9;

11 GSLRXCKXKXGSPFXARXIFKDAKTKLFWISYSDGDCASSPCQNGSGCKDOLQSYC 70  
 12 GMLRECKREKESFEARREVFETETEFWQYVGDGDCSPCLNGCMCKNDINSYC 71  
 71 PCLPFEKNCETHMDOLICVNEGGCGQYQSDHTGTRSCRCHEGYSILADSVCTPT 130  
 72 WQAGFEKNCCL---DATCSIKNGKCKQFCKRDNDNVVSCDTGYRLAEDQKCEPA 127  
 131 VEPGCKTPI--LEK---NASKP-----GATYGVK 158  
 138 VFFPGGRVSVSISKLLKRAETIFSTNTYNSSESAIINDNTQSNQSFDESRVVGDD 187  
 159 CPKGCPCMVOLLVNGAQLCGTLINTIIVVSAACFCDKIKMNRNLIAVGEHLSSEHG 218  
 188 AERGFPMQVLLHGEIAAFCCGSIVNEKVVTAHC---IKRGVKTIVVAGENHTKPEP 244  
 219 DEQSRVAOVITPSTYVET---NHDIALLRHQVPLVDHVVPLCLPERTSEKRLAVY 276  
 245 TEQKRNVAIRAIYHSYNASINKYSHDIALLEDEPLELSYVPICIADRDY---TNIPS 301  
 277 RF--SLVSGMGLDGAATALMLVNLVRLMTQDCLQDSKRVGSDPNTTEVFCAGYSD 334

Db 302 KFGYVSGMGKVFNRGRSASIILOYLKPLVDRATCLRSTK-----SIYSHMFCAGYHE 356  
 Oy 335 GSKDCGDSGGPAPHATYRGWTLTGIVSGGCGATGHHGVYTRVSOYLEMOK 389  
 357 GGRDCGDSGGPAPHATYRGWTLTGIVSGGCGATGHHGVYTRVSOYLEMOK 411  
 Db 357 GGRDCGDSGGPAPHATYRGWTLTGIVSGGCGATGHHGVYTRVSOYLEMOK 411

RESULT 7  
 KFHU  
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human  
 N:Alternate names: antithrombin factor B; Christmas factor  
 C:Species: Homo sapiens (hmn)  
 C:Date: 17-Dec-1982 #sequence, revision 30-Jun-1987 #text, change 15-Sep-2000  
 C:Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486;  
 R:Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.  
 Biochemistry 24, 3736-3750, 1985  
 A:Title: Nucleotide sequence of the gene for human factor IX (antithrombin factor B  
 A:Reference number: A00922; PMID:86000558; PMID:2994716  
 A:Accession: A00922  
 A:Molecule type: DNA  
 A:Residues: 1-461 <YOS>  
 A:Cross-references: GB:K02402; NID:q182612; PIND:AB59620.1; PID:q182613  
 R:Rason, D.S.; Choo, K.H.; Rees, D.J.G.; Glanville, F.; Gould, K.; Huddleston, J.A.;  
 EMBO J. 3, 1053-1060, 1984  
 A:Title: The gene structure of human anti-haemophilic factor IX  
 A:Reference number: A37570; PMID:84236100; PMID:6329724  
 A:Accession: A37570  
 A:Molecule type: DNA  
 A:Residues: 1-461 <ANS>  
 A:Cross-references: GB:K02048  
 R:Reisma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.  
 Blood 72, 1074-1076, 1988  
 A:Title: The putative factor IX gene promoter in hemophilia B Leyden.  
 A:Reference number: A30511; PMID:88327116; PMID:3416069  
 A:Accession: A30511  
 A:Molecule type: DNA  
 A:Residues: 8-24 <REX>  
 A:Cross-references: EMBL:X55008; NID:q311288; PIND:CA838245.2; PID:g4469253  
 R:Koeberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.  
 Am. J. Hum. Genet. 45, 448-457, 1989  
 A:Title: Functionally important regions of the factor IX gene have a low rate of poly  
 A:Reference number: A32989; PMID:89317152; PMID:2773937  
 A:Accession: A32989  
 A:Molecule type: DNA  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 30-92 <ROE>  
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985  
 A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagu  
 A:Reference number: A22673; PMID:85190593; PMID:3857619  
 A:Accession: A22673  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', '195-461 <MCG>  
 A:Cross-references: GB:M11309; NID:q180552; PIND:AAA52023.1; PID:q180553  
 A:Note: the authors translated the codon ACA for residue 29 as Tyr  
 R:Daye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohl, V.; Flindell, A.; Tolst  
 Nucleic Acids Res. 11, 2325-2335, 1983  
 A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52  
 A:Reference number: A21337; PMID:83220788; PMID:6687940  
 A:Accession: A21337  
 A:Molecule type: mRNA  
 A:Residues: 1-193, 'T', '195-461 <JAV>  
 A:Cross-references: GB:J00137; NID:q182610; PIND:AAA52763.1; PID:q182611  
 R:Jagdevan, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.  
 Somat. Cell Mol. Genet. 10, 465-473, 1984  
 A:Title: Isolation and characterization of human factor IX cDNA: identification of Ta  
 A:Reference number: A37546; PMID:84300526; PMID:6089357  
 A:Accession: A37546  
 A:Molecule type: mRNA  
 A:Residues: 38-193, 'T', '195-326 <JAG>  
 A:Cross-references: GB:M35672  
 R:Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982

A:Title: Isolation and characterization of a cDNA coding for human factor IX.  
A:Reference number: A30623; MUID:83065193; PMID:6959130  
A:Accession: A30623  
A:Molecule type: mRNA  
A:Residues: 1-12, 'S', '14-73, 'P', '75-82, 'K', '84-203, 'P', '205-216, 'G', '218-298, 'A', '299-356, 'A', 'A:Cross-references: GB:J00136; NID:9182608; PIDN:AAA98726.1; PID:9182609  
A:Experimental source: liver  
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
Vox Sang. 58, 21-29, 1990  
A:Title: Development of an immunofluorescent process for factor IX purification.  
A:Reference number: A60486; MUID:90194857; PMID:2316207  
A:Accession: A60486  
A:Molecule type: protein  
A:Residues: 47-52, 'XX', '55-60, 'X', '62, 'XX', '65 <THA>  
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors.  
A:Reference number: A20274; MUID:83308813; PMID:6685526  
A:Accession: A20274  
A:Molecule type: protein  
A:Residues: 105-109, 'X', '111-115 <MCM>  
R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle, Eur. J. Biochem. 172, 565-572, 1988  
A:Title: Characterisation of two differently processed forms of human recombinant factor IX.  
A:Reference number: S02527; MUID:88166735; PMID:3280312  
A:Accession: S02527  
A:Molecule type: protein  
A:Residues: 29-63 <BAL>  
A:Note: processed forms expressed in recombinant system  
R:Ballat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dlesterle, A.; Faure, T.; Meullen, EMO J. 9, 3295-3301, 1990  
A:Title: Characterization of recombinant human factor IX expressed in transgenic mice at A:Reference number: S12058; MUID:91006024; PMID:2209546  
A:Accession: S12058  
A:Molecule type: mRNA; protein  
A:Residues: 1-68 <JAL>  
A:Note: processed forms expressed in recombinant system  
R:Handford, P.A.; Barron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campb EMO J. 9, 475-480, 1990  
A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium A:Reference number: S12377; MUID:90151623; PMID:2406129  
A:Accession: S12377  
A:Molecule type: protein  
A:Residues: 92-130 <HAN>  
A:Note: NMR detection of calcium binding by domain expressed in recombinant system  
R:de la Salle, C.; Charmanlier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum, Thromb. Haemost. 70, 370-371, 1993  
A:Title: A deletion located in the 3' non translated part of the factor IX gene respons A:Reference number: I59612; MUID:94054330; PMID:8236130  
A:Accession: I59612  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 444-461 <RES>  
A:Cross-references: GB:S66752; NID:9439773; PIDN:AA8588.1; PID:9439774  
R:Stoffel, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.  
Science 239, 491-494, 1988  
A:Title: Genomic amplification with transcript sequencing.  
A:Reference number: I59529; MUID:88127096; PMID:3340835  
A:Accession: I59529  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 290-359 <RE2>  
A:Cross-references: GB:M19063; NID:9182622; PIDN:AAA52456.1; PID:9182623  
R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin A:Reference number: A54255; MUID:94227047; PMID:8172892  
A:Accession: A54255  
A:Molecule type: protein  
A:Residues: 'D', '204, 'X', '206-211, '212, 'D', '214, 'X', '216-221, 'D', <AG2>  
A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.  
J. Clin. Invest. 61, 1528-1538, 1978

A:Title: Activation of human factor IX (Christmas factor).  
A:Reference number: A16483; MUID:78194509; PMID:659613  
A:Contents: annotation; activation; active site; carbohydrate binding  
R:McGraw, R.A.; Davy, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D. Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984  
A:Reference number: A37569  
A:Contents: annotation  
A:Note: 194-Thr was also found  
R:Mortla, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
J. Biol. Chem. 259, 5698-5704, 1984  
A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-bi A:Reference number: A37543; MUID:84185715; PMID:6425296  
A:Contents: annotation; calcium binding  
R:Mortla, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
J. Biol. Chem. 260, 2583, 1985  
A:Reference number: A37544  
A:Contents: annotation; calcium binding, correction  
R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
Cell 45, 343-348, 1986  
A:Title: Defective propeptide processing of blood clotting factor IX caused by muta A:Reference number: A37545; MUID:86189947; PMID:3009023  
A:Contents: annotation; signal sequence cleavage site  
R:Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Ka J. Biol. Chem. 264, 21257-21265, 1989  
A:Title: Blood clotting factor IX (F9) Nagoya: substitution of arginine 180 by trypt A:Reference number: A30622; MUID:90078229; PMID:2593373  
A:Contents: annotation; sequence of mutant (F9) Nagoya  
R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Br submitted to the Brookhaven Protein Data Bank, November 1991  
A:Reference number: A51252; PDB:1IXA  
A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
A:Note: recombinant form expressed in yeast  
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptid C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vita C:Genetics:  
A:Gene: GDB:F9  
A:Cross-references: GDB:119900; OMIM:306900  
A:Map position: Xq27.1-Xq27.2  
A:Intons: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
A:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the p C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homo F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-46/Domain: propeptide #status experimental <PPT>  
F:31-91/Domain: Gla domain homology <GLA>  
F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>  
F:97-128/Domain: EGF homology <EGF>  
F:134-170/Domain: EGF homology <EG2>  
F:192-226/Domain: activation peptide #status experimental <ACT>  
F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
F:227-454/Domain: trypsin homology <TRY>  
F:53, 54, 61, 63, 66, 67, 72, 73, 76, 79, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu F:64-69, 97-108, 102-117, 119-128, 134-145, 141-155, 157-170, 178-335, 252-268, 382-396, 407-4 F:94/Binding site: carboxylate (Ser) (covalent) #status experimental  
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:191-192/Cleavage site: Arg-Ala (coagulation factor XIa) #status experimental  
F:203, 213/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:205, 215/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:226-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental

Query Match 38.8%; Score 849; DB 1; Length 461;  
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Matches 161; Conservativity 71; Mismatches 132; Indels 50; Caps 7;  
QY 11 GSLRXKXKXQCSFXXARXIFKDXRTKFTWYSYSGDCASPCQNGSSCKDQLOSLYC 70  
DB 58 GNLRECKHEKESFEAREVFEFTERTTFEMQYVDGDCESPCNLGSKDDINSYSC 117  
QY 71 FLPAFEGRNCTETKDDOLICVNGGCEQYCSDHGTGRSCRCHEGYSLADGVSCPT 130

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Db      118 MCFPEFEGNCEL-----DYTCNKNGRCQFCKNSADNKNVSCSTGYALAEOKSCFEA 173
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Qy      160 PKGCEPMOVLILVNAOJCGGLINTIYVYSAHCFDKKNNRLAVIGEEDLSHDD 219
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Qy      220 EQRRAVAVIIPSTVYVPGT--NHDIALLRHQPVYLDTHVYPLCPERTFERTLAFFR 277
Db      291 EQRRAVAVIIPSTVYVPGT--NHDIALLRHQPVYLDTHVYPLCPERTFERTLAFFR 277
Qy      278 F--SLVSGMGLLDGAFALVLEMLVNPRLMTQDLQOSRKVSDPENTYMFCAAGSDG 335
Db      348 FGSYGVSQMGVRFHGRSALVLYQVLRVPLVDRATCRSTK-----TIVNNKFCAGFHGG 402
Qy      336 SKDSCGSGGPHAHYRGTWLTGIVSGGCAVYGHGVYTRVSOIYEMJCK 389
Db      403 GRDSCGSGGPHAHYRGTWLTGIVSGGCAVYGHGVYTRVSOIYEMJCK 389

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## RESULT 8

EXBO

coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N:Alternate names: Stuart factor

C:Species: Bos primigenius taurus (cattle)

C:Date: 24-Apr-1984 #sequence-revision 17-Mar-1987 #text-change 16-Jul-1999

C:Accession: A22867; A14997; A12030; A34412; S39414; A00925

R:Func: M.R.; Campbell, R.M.; McGillyray, T.A.

Nucleic Acids Res. 12, 4481-4492, 1984

A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a

A:Reference number: A22867; MUID:84247315; PMID:6330671

A:Accession: A22867

A:Molecule type: mRNA

A:Residues: 1-487 &lt;FNU&gt;

A:Cross-references: GB:X00673; MID:g192; PID:CAA25286.1; PID:g193

R:Entrez: D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).

A:Reference number: A14997; MUID:80130563; PMID:6766735

A:Accession: A14997

A:Molecule type: protein

A:Residues: 41-102, N, 104-180 &lt;ENF&gt;

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; MUID:83308813; PMID:6688526

A:Accession: A20274

A:Molecule type: protein

A:Residues: 41-102, N, 104-180 &lt;ENF&gt;

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; MUID:83308813; PMID:6688526

A:Accession: A20274

A:Molecule type: protein

A:Residues: 41-102, N, 104-180 &lt;ENF&gt;

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; MUID:83308813; PMID:6688526

A:Accession: A20274

A:Molecule type: protein

A:Residues: 41-102, N, 104-180 &lt;ENF&gt;

R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; MUID:83308813; PMID:6688526

A:Accession: A20274

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A:Residues: 183-196,199-209,216-233 <INO>
A>Note: carbohydrate binding sites
R:Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Biochemistry 11, 4899-4903, 1972
A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mam
A:Reference number: A1453; MUID:73053314; PMID:4264286
A:Accession: A1453
A:Contents: annotation; active site
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha
A:Reference number: A13504; MUID:76053121; PMID:1059122
A:Contents: annotation; activation
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxygluta
A:Reference number: A38024; MUID:84185716; PMID:6546930
A:Accession: A38024
A:Contents: annotation; calcium binding
J. Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A:Reference number: A38025; MUID:86140210; PMID:3949800
A:Accession: A38025
A:Contents: annotation; sulfate binding
C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C:Comment: The two chains are formed from a single-chain precursor by the excision of
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)
activation.
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita
A:Gene: F10
A:Map position: 13q34
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-15/Domain: signal sequence #status predicted <PRO>
F:16-40/Domain: Gla domain homology <GLA>
F:41-180/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
F:183-233/Domain: activation peptide #status experimental <APP>
F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F:234-461/Domain: trypsin homology <TRY>
F:46-47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu)
F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #statu
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F:208/Binding site: sulfate (Tyr) (covalent) #status experimental
F:208/485/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:233-234/Cleavage site: Arg-Tile (coagulation factor IXa, coagulation factor VIIa) #s
F:240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
F:275,321,418/Active site: His, Asp, Ser #status predicted

```

```

Query Match      38.5% Score 843: DB 1: Length 492;
Best Local Similarity 37.7% Pred. No. 2.2e-55;
Matches 165: Conservative 70; Mismatches 147; Indels 56; Gaps 7;

```

```

Qy      1 ANAFLXLRPGLSRKCKXKXOCFFXXARXIFKXAKRKLFWISYSDQACASSPCQNGS 60
Db      41 ANSFLXLRPGLSRKCKXKXOCFFXXARXIFKXAKRKLFWISYSDQACASSPCQNGS 100
Qy      61 CKDQLOSLICFCLAFGRNCEHKKDQDLIVNNGGCEQCSHTGTGKSCRHEGYSL 120
Db      101 CKDQLOSLICFCLAFGRNCEHKKDQDLIVNNGGCEQCSHTGTGKSCRHEGYSL 157
Qy      121 LADGVSCTPYVEYPCGKPILEK-----RIVGKVC 144
Db      158 GDDSKSCVSTFRFCGAFQGRSRRAHISSEDLASLEHDPADLSPESLDDLGL 217
Qy      145 NASRPGQ-----RIVGKVC 195

```



Db 218 NRTEPSAGEDSGQVRIIVGRDCAEGCEPMQALLVNEENEGFCGTLINERYVTAACHL 277  
 Qy 196 DKINMRNLIVLSEHDLSEHDEDSRRVAQVIIPSTYVPGTNNHIALRLHQPVL 255  
 Db 278 HQARF---TVRVDRNTEDEGENMAHEVMTAKHSFVETDFOIALRLTPIPR 334  
 Qy 256 DHVPLCLPRTFERTSLAFVRFSLVSGWGLDRGATALEMLVNPRLMTODCLOQSR 315  
 Db 335 RNVAAPCLPEKOMAEATLMTOKTGVSGFGTHRGRLSSTLKLTPYVDRSTC----- 389  
 Qy 316 KVGDSPNTEYMFACAGSDGSKDSCGPHATHTRGVTLGTVSGWGCATVGHFG 375  
 Db 390 KLSSFTITPMFCAGSDTQPEDDCOGDSGPHATHTRGVTLGTVSGWGCATVGHFG 449  
 Qy 376 YTRVSOYIEMLOKLRMS 393  
 Db 450 YTKVSNFLKWKIDRKMA 467

## RESULT 9

## EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #text\_change 08-Dec-2000  
 C:Accession: S49075; J04670; PS0191; PS0190; 162745  
 R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.  
 Thromb. Res. 80, 63-73, 1995  
 A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra  
 A:Reference number: A58498; MUID:96093366; PMID:8578539  
 A:Accession: S49075  
 A:Molecule type: mRNA  
 A:Residues: 1-482 <STAL>  
 A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
 A>Note: submitted to the EMBL Data Library, June 1994  
 A>Note: neither the complete nucleic acid sequence nor the complete translation are shown  
 R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.  
 Gene 169, 269-273, 1996  
 A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
 A:Reference number: J04670; MUID:96194815; PMID:8647460  
 A:Accession: J04670  
 A:Molecule type: mRNA  
 A:Residues: 1-482 <STAL>  
 A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
 A:Experimental source: Cos-1 cell  
 R:Enjyoji, K.; Miyazaki, K.; Kato, H.  
 J. Biochem. 109, 890-898, 1991  
 A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla  
 A:Accession: PS0191  
 A:Reference number: PS0190; MUID:92041742; PMID:1718949  
 A:Molecule type: protein  
 A:Residues: 41-58 'X', 60-65 <ENJ1>  
 A:Accession: PS0190  
 A:Molecule type: Protein  
 A:Residues: 183-186 'X', 188-207 <ENJ2>  
 R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
 Eur. J. Haematol. 52, 162-166, 1994  
 A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
 A:Reference number: I6196; MUID:94222160; PMID:8168596  
 A:Accession: I6196  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 295-383, 'G', 385-455 <MUR>  
 A:Cross-references: GB:D21215; NID:g415309; PIDN:BA04756.1; PID:g455396  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamat  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: signal sequence #status predicted <SIG>  
 F:25-84/Domain: Gla domain homology <Gla>  
 F:41-179/Product: coagulation factor X light chain #status predicted <LCH>  
 F:190-121/Domain: EGF homology <EG1>

F:129-164/Domain: EGF homology <EG2>  
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F:183-231/Domain: activation peptide #status predicted <APT>  
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F:232-482/Domain: trypsin homology <TRY>  
 F:46-47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #  
 F:56-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-40  
 F:187/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:187/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:208/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F:218/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:231-232/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #  
 F:274,320,417/Active site: His, Asp, Ser #status predicted

Query Match 38.08; Score 831.5; DB 1; Length 482;  
 Best Local Similarity 36.14; Pred. No. 1.6e-54;  
 Matches 159; Conservative 83; Mismatches 144; Indels 55; Gaps 7;

Qy 1 ANAFLLXLRPGSLRXKCKKXQSEFXARXFKAXTKLFWISPDGDCASSPCONGS 60  
 Db 41 ANSFEEIKKGNLERECVEICFEEARREVEEDNETTERWKNYEDGDCSSPCONGE 100  
 Qy 61 CKDOLSYICFLPAFEGNCEFHKKDQILCVENGCCEQYSDHTGTRSCCHGYSL 120  
 Db 101 CRDGLSYCTCTEGFEGKNCLEFV--RLKSLDNDCQFCNEQNSV-VSCAKGYFL 157  
 Qy 121 LADGVSCTPTVEPCSKT-----PILEKR 144  
 Db 158 GNDGKSLSTAFPFCKTKTKRAKRSVALNTSNSEPPDPLMDPADILVPTSPSLNL 217  
 Qy 145 NASKPQ-----RIYGVKCPKGECPMOLLVYNAQ--LCGGLINTIYVSAHCFD 196  
 Db 218 KTEPEANSDVIRIYGGGCKRGCEPMQALLFSEETGDFGCGTILNEFYILTAHCLH 277  
 Qy 197 KIKMNRNLIVLSEHDLSEHDEDSRRVAQVIIPSTYVPGTNNHIALRLHQPVLTD 256  
 Db 278 QAKRFK---VRVGDLTNEDEGGEVMEVDMLIKHKRFRDYYEDIALRLKTPITRE 334  
 Qy 257 HVPPLCLPRTFERTSLAFVRFSLVSGWGLDRGATALEMLVNPRLMTODCLOQSR 316  
 Db 335 RNVAAPCLPEKOMAEATLMTOKTGVSGFGTHRGRLSSTLKLTPYVDRSTC-----R 389  
 Qy 317 KVGDSPNTEYMFACAGSDGSKDSCGPHATHTRGVTLGTVSGWGCATVGHFG 376  
 Db 390 LSTSFSTIYNMFCAGSDTQPEDDCOGDSGPHATHTRGVTLGTVSGWGCATVGHFG 449  
 Qy 377 YTRVSOYIEMLOKLRSEPR 397  
 Db 450 YTKVTAFLKWKIDRSMAKRVGP 470

## RESULT 10

coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999  
 C:Accession: J00419; I49667  
 R:Wu, S.M.; Stafford, D.W.; Ware, J.  
 Gene 86, 275-278, 1990  
 A:Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.  
 A:Reference number: J00419; MUID:90215309; PMID:2325576  
 A:Accession: J00419  
 A:Molecule type: mRNA  
 A:Residues: 1-459 <WUS>  
 A:Cross-references: GB:M23109; NID:g193317; PIDN:AAJ37629.1; PID:g387158  
 A:Experimental source: liver  
 R:Sarkar, G.; Koehler, D.D.; Sommer, S.S.  
 Genomics 6, 133-143, 1990  
 A:Title: Direct sequencing of the activation peptide and the catalytic domain of the  
 A:Reference number: I46580; MUID:90152675; PMID:2303254  
 A:Accession: I49667  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA



A:Residues: 168-362, 'O', 364-387, 'I', 389-451 <RES>  
 A:Cross-references: GB:M6236; NID:9193319; PIDN:AAA7630.1; PID:9193320  
 A:Molecule type: mRNA  
 A:Residues: 1-452 <AXE>  
 A:Cross-references: GB:M3826; NID:9163949; PIDN:AAA30844.1; PID:9163950  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
 F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:17-34/Domain: propeptide #status predicted <PRO>  
 F:19-79/Domain: Gla domain homology <Gla>  
 F:35-453/Product: coagulation factor IX #status predicted <MAT>  
 F:85-116/Domain: EGF homology <EG2>  
 F:122-158/Domain: EGF homology <EG2>  
 F:41-42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxyglutamic acid (Glu) #  
 F:52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,230-265,380-394,405-433/Di  
 F:265,313,409/Active site: His, Asp, Ser #status predicted

Query Match 37.7%; Score 824; DB 2; Length 459;  
 Best Local Similarity 39.3%; Pred. No. 5,4e-54;  
 Matches 169; Conservative 57; Mismatches 132; Indels 72; Gaps 10;

11 GSLRXKXXKXGCSFXXARXIFKDAKRTKLEWISYSDGQCASSPQNGSGCKDQLOSYIC 70  
 46 GNLEKCEIEKCSFEDEAEVEFENETKTEFEWKQYVDGQCESNPLNDGVCKDDINSYEC 105  
 71 FCLPAFEGNCEETHRDQDLICVNEGCEQYCSDHGTGKRSRCHEGYSLADGVSCPT 130  
 106 WQVGFEGKNCNL-----DVTGNKNGRCKQFCNPKNVICSCTEGYQLAEDQSCPT 161  
 131 VEYPCGKIPI-----LEKRNASKP 149  
 162 VPFCNGRASISYSSKKTIRATFVSNDYENSTEVEFIDDTGAILNNTSESSESLND 221  
 150 QGRVKGKVCCKGCPQVOLLVNGAQLCGTILNTIIVWSAHC-----DKIKMRNLIA 206  
 222 FTRVYGEKNAKPGQIPQVILNGEIEAFCCGAILNEKIYIAAHCCKGDMIE-----V 275  
 207 VLGHDLSEHDGDSQSRVAQVITPSTYVPGTIN---HDILRLHQPVLTDHVPVLCPEPTFSERTLA 263  
 276 VAGYINLNDKEDTEQRRNRVHT-IPHQYNATINKYSHDIALLEDKPLINSYVTPICV 334  
 264 PERTFSERTLAFAVF--SLVSGMQLDRGATALELWLVNPLMTQDCLQOSRKVGDSP 321  
 335 ANR---EYTNIFLKFGSGYVSGMGRVFNKGRHNSILQYLRPLVDRATCLR-----ST 384  
 322 NITEY--MFCAGYSDGSKDSCGSGPRHATYRGTYWLTGIVSGGCGATVGHGVTYR 379  
 385 TETTYNNMFCAGYREGGKDCSGDSDGSPHYTEVEGTSTLTGIIISGECAMKXGIVTK 444  
 380 VSOYIEMLOK 389  
 445 VSRIVNMIKE 454

## RESULT 11

A30351  
 coagulation factor IXa (EC 3.4.21.22) precursor - dog  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999  
 C:Accession: A30351; 146201  
 R:Evans, J.P.; Matzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.  
 Blood 74, 207-212, 1989  
 A>Title: Molecular cloning of a cDNA encoding canine factor IX.  
 A:Reference number: A30351; MUID:8932338; PMID:2752110  
 A:Accession: A30351  
 A:Molecule type: mRNA  
 A:Status: preliminary  
 A:Residues: 1-452 <EVA>  
 A:Cross-references: GB:M2157; NID:9972719; PIDN:AAA75006.1; PID:9163948  
 R:Axelrod, J.H.; Read, M.S.; Brinkhaus, K.M.; Verma, I.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990  
 A>Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilid  
 A:Reference number: 146201; MUID:90311364; PMID:2367523  
 A:Accession: 146201

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-452 <AXE>  
 A:Cross-references: GB:M3826; NID:9163949; PIDN:AAA30844.1; PID:9163950  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-40/Domain: propeptide #status predicted <PRO>  
 F:24-84/Domain: Gla domain homology <Gla>  
 F:41-452/Product: coagulation factor IX #status predicted <MAT>  
 F:90-121/Domain: EGF homology <EG2>  
 F:127-163/Domain: EGF homology <EG2>  
 F:218-445/Domain: trypsin homology <TRY>  
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu)  
 F:57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-255,373-387,398-426  
 F:258,306,402/Active site: His, Asp, Ser #status predicted

Query Match 37.5%; Score 821; DB 1; Length 452;  
 Best Local Similarity 39.5%; Pred. No. 8,8e-54;  
 Matches 163; Conservative 67; Mismatches 133; Indels 50; Gaps 10;

11 GSLRXKXXKXGCSFXXARXIFKDAKRTKLEWISYSDGQCASSPQNGSGCKDQLOSYIC 70  
 51 GNLEKCEIEKCSFEDEAEVEFENETKTEFEWKQYVDGQCESNPLNDGVCKDDINSYEC 110  
 71 FCLPAFEGNCEETHRDQDLICVNEGCEQYCSDHGTGKRSRCHEGYSLADGVSCPT 130  
 111 WQVGFEGKNCNL-----DVTGNKNGRCKQFCNPKNVICSCTEGYQLAEDQSCPT 166  
 131 VEYPCGKIPI-----LEKRNASKP 161  
 167 VPFCNGRASISYSSKKTIRATFVSNDYENSTEVEKILDNVOTQDLNFTRVGSKDAKP 226  
 162 GECQPMOVLVNGAQLCGTILNTIIVWSAHC-----DKIKMRNLIAVCEHDLSEHDCDE 220  
 227 GQFPMQVLNCKVDACGSGSIENKRVYTAACCEPDVK---ITIVGHNTEKREHTE 282  
 221 QSRVAVQVITPSTY--VGTNTHDIALRLHQPVLTDHVPVLCPEPTFSERTLAFAVF 278  
 283 QKRVNITILHNSVATINKYSHDIALLEDEPLDNLNSYVTPICADAEYSN---IFLKF 339  
 279 --SLVSGMQLDRGATALELWLVNPLMTQDCLQOSRKVGDSPNITEYFCAGYSDSP 336  
 340 GSGYVSGMGRVFNKGRHNSILQYLRPLVDRATCLRSTK-----TIYNNFCAGFHEG 394  
 337 KDCSGDSCGPRHATYRGTYWLTGIVSGGCGATVGHGVTYRQYIEMLOK 389  
 395 KDCSGDSCGPRHATYRGTYWLTGIVSGGCGATVGHGVTYRQYIEMLOK 447

## RESULT 12

184615  
 coagulation factor VII - rhesus macaque (fragment)  
 C:Species: Macaca mulatta (rhesus macaque)  
 C:Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 22-Jun-1999  
 C:Accession: 184615  
 R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
 Eur. J. Haematol. 52, 162-168, 1994  
 A>Title: Analysis of the partial nucleotide sequences and deduced primary structures  
 A:Reference number: 146196; MUID:94222160; PMID:8168596  
 A:Accession: 184615  
 A:Molecule type: DNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-159 <RES>  
 A:Cross-references: GB:D2122; NID:9415306; PIDN:BA04753.1; PID:9455394  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 F:1-159/Domain: trypsin homology (fragment) <TRY>  
 Query Match 35.7%; Score 781; DB 2; Length 159;  
 Best Local Similarity 91.8%; Pred. No. 3e-31;  
 Matches 146; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

215 EHDDEQDSRRVAVQVITPSTYVPGTTHDIALRLHQPVLTDHVPVLCPEPTFSERTLA 274

```

Db      1 EHEGDEQSRRAVQVPIIPSTYVGLATNNDLALLRLQGPVLTIDHVPFLCLPEMSERTLA 60
      275 FVRFSLVSGWGLDRLGATLALVLPRLMTQDCLQOSRRVGDSPNITEYMFAGYSD 334
      61 FVRFSLVSGWGLDRLGATLALVLPRLMTQDCLQOSRRVGDSPNITEYMFAGYSD 120
Oy      335 GSKDSCKDGSGGPHATHTYRTWLTGIVSGWGGCAVNGH 373
      121 GSRDSCKDGSGGPHATHTYRTWLTGIVSGWGGCAVNGH 159

```

## RESULT 13

```

S18994
protein C (activated) (EC 3.4.21.69) precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C.Accession: S18994; S24312
R.Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A.Description: The cDNA cloning and mRNA expression of rat protein C.
A.Reference number: S18994
A.Accession: S18994
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-461 <OKA>
A.Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
R.Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A.Title: The cDNA cloning and mRNA expression of rat protein C.
A.Reference number: S24312; MUID:92329550; PMID:1627650
A.Accession: S24312
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-461 <OKA>
A.Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
R.Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A.Title: The cDNA cloning and mRNA expression of rat protein C.
A.Reference number: S24312; MUID:92329550; PMID:1627650
A.Accession: S24312
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-461 <OKA>
A.Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology
C.Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F.1-32/Domain: signal sequence #status predicted <SIG>
F.32-85/Domain: Gla domain homology <Gla>
F.33-42/Domain: propeptide #status predicted <PRO>
F.43-461/Product: protein C #status predicted <PC>
F.91-130/Domain: EGF homology <EG1>
F.139-174/Domain: trypsin homology <EG2>
F.213-445/Domain: EGF homology <EG2>
F.47-48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F.112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F.121-130,139-150,146-159,161-174,182-320,323-255,373-387,398-426/Disulfide bonds: #stat
F.215,291,355/Binding site: carboxydrate (Asn) (covalent) #status predicted
F.254,300,402/Active site: His, Asp, Ser #status predicted

```

```

Query Match      35.4%; Score 775; DB 1; Length 461;
Best Local Similarity 37.7%; Pred. No. 2.4e-50;
Matches 164; Conservative 67; Mismatches 156; Indels 48; Gaps 11;

```

```

Oy      1 ANAFLLXLRPGSLKRXCKXKXCSFXAXRIFKDXARTLFIWISYSDGQCS----- 52
      42 ANSFLLEKRPASLEKRECEIEICDFEAEQEIIONVEDTIAFWIKRIFKDFGQCCSTPLDHCD 101
      53 SPCONGSGCKDQLOSLYICFLPAFGRNCETHKDDQLICVNEGCGEYCGSDHTGTRSC 112
      102 SPCGHGTCIDIGLGFSCDCKGWGRCCQDEMPG-DCKRVKNGGCHYCLETRGR-C 159
      113 RCHGEGSLADGVSCSTPVEYPCGKIPLEKRNASKPOG-----RIVGG 156
      160 RCAGGYELADDDHMKCRPVNFPCK---LAKRTDKKRNKFRDIDPEDELELPRIYNG 216
      157 KVCPRGECPRQVLLVNGAOL-CGGTLINTIWWVSAACFPKIKMRLIAVLGEHDLSE 215
      217 TLTKGGSPQWAILLDSKKKLACGVLHTSWVLAACLESSR---KLTVRLGEYDLRR 273
      216 HDGDSQSRRAVQVPIIPSTYVGLATNNDLALLRLQGPVLTIDHVPFLCLPERTFSERTLA 275

```

```

Db      274 RDPWELODIREVLVHPNTRNSNDLALLRLSPATLSKTIPTICLPNSGLAELLSOA 333
      276 VRFSLVSGWGLD-----RGATLALVLPRLMTQDCLQOSRRVGDSPNITEYMF 329
      334 GQETVTVGKGVQSDKVKQDGRNRRTFI-LTFITPLAARDCHQVNNV-----VSENNMC 387
Oy      330 AGVSQSGKDSCKDSCGSGGPHATHTYRTWLTGIVSGWGGCAVNGHGVYTRVQYIEWLQK 389
      388 AGIIGDTRACDGDGSGGPHATHTYRTWLTGIVSGWGGCAVNGHGVYTRVQYIEWLQK 447
Oy      390 LMRSEPRGVLLRAP 404
      448 YIGER---DYSLSKP 459

```

## RESULT 14

```

JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N.Alternate names: vitamin K-dependent serine proteinase
C.Species: Mus musculus (house mouse)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C.Accession: JX0210
R.Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A.Title: Isolation and characterization of a mouse protein C cDNA.
A.Reference number: JX0210; MUID:92316897; PMID:1618739
A.Accession: JX0210
A.Molecule type: mRNA
A.Residues: 1-461 <TAD>
A.Cross-references: GB:D10445; NID:g220385; PIDN:BA01235.1; PID:g220386
A.Experimental source: liver.
C.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that
s.
C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol
C.Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F.1-33/Domain: signal sequence #status predicted <SIG>
F.32-85/Domain: Gla domain homology <Gla>
F.33-41/Domain: propeptide #status predicted <PRO>
F.42-196,199-461/Product: protein C #status predicted <PC>
F.91-130/Domain: EGF homology <EG1>
F.139-174/Domain: EGF homology <EG2>
F.199-461/Domain: heavy chain #status predicted <PC>
F.199-211/Domain: activation peptide #status predicted <ACT>
F.212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIR>
F.213-445/Domain: trypsin homology <TRY>
F.47-48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F.112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F.121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #s
F.215,290,355/Binding site: carboxydrate (Asn) (covalent) #status predicted
F.253,299,402/Active site: His, Asp, Ser #status predicted

```

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Query Match      35.2%; Score 769; DB 1; Length 461;
Best Local Similarity 36.9%; Pred. No. 6.8e-50;
Matches 159; Conservative 80; Mismatches 150; Indels 42; Gaps 12;

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Oy      1 ANAFLLXLRPGSLKRXCKXKXCSFXAXRIFKDXARTLFIWISYSDGQCS----- 52
      42 ANSFLLEKRPASLEKRECEIEICDFEAEQEIIONVEDTIAFWIKRIFKDFGQCCAPPLDHCD 101
      53 SPCONGSGCKDQLOSLYICFLPAFGRNCETHKDDQLICVNEGCGEYCGSDHTGTRSC 112
      102 SPCGHGTCIDIGLGFSCDCKGWGRCCQDEMPG-DCKRVKNGGCHYCLETRGR-C 159
      113 RCHGEGSLADGVSCSTPVEYPCGKIPLEKRNASKPOG-----POGRIVGAKCP 160
      160 ACAGGYELADDDHMKCRPVNFPCK---LLEKRNASK-----POGRIVGAKCP 219
      161 KGCPRQVLLVNGAOL-CGGTLINTIWWVSAACFPKIKMRLIAVLGEHDLSEHGD 219
      220 QGDSPPQWAILLDSKKKLACGVLHTSWVLAAC---VEETKLTLYRLGSDYDLRRDHW 276
      220 EQSRRAVQVPIIPSTYVGLATNNDLALLRLQGPVLTIDHVPFLCLPERTFSERTLA 278

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Db      277  ELDLDIKELVHPNTRYRSSDDNDIALRLAQPATLSKTIYPICLPNNGLAQJELTOAQOE 336
OY      279  SLVSGMGGLD-----RGATALEMLVNLVPRMATDCCLOQSKRVGDSPIITEYFCAGY 332
Db      337  TVYVGMGQSDRIKQGRNRRTPI-LTFIRIPIPLVARNCEVEVMNV-----VSEMLCAGI 390
OY      333  SDGSKDSCRGDSGGPHATHYRGTWLTGIVSGQGCAFGHFGVTVRVSOYIEMLOKLMR 392
Db      391  IGNFTDADCDDGGSGPMNVFFRGTWELVGLVSGEGCGHNNNYOITYTKVSGYLWIMHSYIG 450
OY      393  SEPRGVLLRA 403
Db      451  EK---GVSLKS 458

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